

<110> Walker, David H.
McBride, Jere W.
Yu, Xue-Jie

<120> Homologous 28-Kilodalton Immunodominant Protein
Genes of *Ehrlichia canis* and Uses Thereof

<130> D6152CIP2/D1

<141> 2002-01-31

<150> 09/660,587
<151> 2000-09-12

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Ser	Thr	Val	Gly	Val	Phe	Gly	Leu	Lys	His	Asp	trp	Asp	Gly	Ser	65	70	75
Pro	Ile	Leu	Lys	Asn	Lys	His	Ala	Asp	Phe	Thr	Val	Pro	Asn	Tyr	80	85	90
Ser	Phe	Arg	Tyr	Glu	Asn	Asn	Pro	Phe	Leu	Gly	Phe	Ala	Gly	Ala	95	100	105
Ile	Gly	Tyr	Ser	Met	Gly	Gly	Pro	Arg	Ile	Glu	Phe	Glu	Ile	Ser	110	115	120
Tyr	Glu	Ala	Phe	Asp	Val	Lys	Ser	Pro	Asn	Ile	Asn	Tyr	Gln	Asn	125	130	135
Asp	Ala	His	Arg	Tyr	Cys	Ala	Leu	Ser	His	His	Thr	Ser	Ala	Ala	140	145	150
Met	Glu	Ala	Asp	Lys	Phe	Val	Phe	Leu	Lys	Asn	Glu	Gly	Leu	Ile	155	160	165
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Leu	Ile	Ser	Met	Phe	Glu	Ala	Thr	Ser	Pro	Lys	Ile	Ser	Tyr	Gln	200	205	210
Gly	Lys	Leu	Gly	Ile	Ser	Tyr	Ser	Ile	Asn	Pro	Glu	Thr	Ser	Val	215	220	225
Phe	Ile	Gly	Gly	His	Phe	His	Arg	Ile	Ile	Gly	Asn	Glu	Phe	Arg	230	235	240
Asp	Ile	Pro	Ala	Ile	Val	Pro	Ser	Asn	Ser	Thr	Thr	Ile	Ser	Gly	245	250	255
Pro	Gln	Phe	Ala	Thr	Val	Thr	Leu	Asn	Val	Cys	His	Phe	Gly	Leu	260	265	270
Glu	Leu	Gly	Gly	Arg	Phe	Asn	Phe								275		

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 Asp Asn Thr Gly Ser Phe Tyr Ile Ser Gly Lys Tyr Val Pro Ser
 35 40 45
 Val Ser His Phe Gly Val Phe Ser Ala Lys Glu Glu Arg Asn Ser
 50 55 60
 Thr Val Gly Val Phe Gly Leu Lys His Asp Trp Asn Gly Gly Thr
 65 70 75
 Ile Ser Asn Ser Ser Pro Glu Asn Ile Phe Thr Val Gln Asn Tyr
 80 85 90
 Ser Phe Lys Tyr Glu Asn Asn Pro Phe Leu Gly Phe Ala Gly Ala
 95 100 105
 Ile Gly Tyr Ser Met Gly Gly Pro Arg Ile Glu Leu Glu Val Leu
 110 115 120
 Tyr Glu Thr Phe Asp Val Lys Asn Gln Asn Asn Asn Tyr Lys Asn
 125 130 135
 Gly Ala His Arg Tyr Cys Ala Leu Ser His His Ser Ser Ala Thr
 140 145 150
 Ser Met Ser Ser Ala Ser Asn Lys Phe Val Phe Leu Lys Asn Glu
 155 160 165
 Gly Leu Ile Asp Leu Ser Phe Met Ile Asn Ala Cys Tyr Asp Ile
 170 175 180
 Ile Ile Glu Gly Met Pro Phe Ser Pro Tyr Ile Cys Ala Gly Val
 185 190 195

Gly Thr Asp Val Val Ser Met Phe Glu Ala Ile Asn Pro Lys Ile		
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Ser Tyr Gln Gly Lys Leu Gly Leu Gly Tyr Ser Ile Ser Ser Glu		
	215	220 225
Ala Ser Val Phe Ile Gly Gly His Phe His Arg Val Ile Gly Asn		
	230	235 240
Glu Phe Arg Asp Ile Pro Ala Met Val Pro Ser Gly Ser Asn Leu		
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Pro Glu Asn Gln Phe Ala Ile Val Thr Leu Asn Val Cys His Phe		
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Asn Ser Met Tyr Gly Asn Phe Tyr Ile Ser Gly Lys Tyr Met Pro		
	35	40 45
Ser Val Pro His Phe Gly Ile Phe Ser Ala Glu Glu Glu Lys Lys		
	50	55 60
Lys Thr Thr Val Val Tyr Gly Leu Lys Glu Asn Trp Ala Gly Asp		
	65	70 75
Ala Ile Ser Ser Gln Ser Pro Asp Asp Asn Phe Thr Ile Arg Asn		
	80	85 90

Tyr	Ser	Phe	Lys	Tyr	Ala	Ser	Asn	Lys	Phe	Leu	Gly	Phe	Ala	Val
			95						100					105
Ala	Ile	Gly	Tyr	Ser	Ile	Gly	Ser	Pro	Arg	Ile	Glu	Val	Glu	Met
			110						115					120
Ser	Tyr	Glu	Ala	Phe	Asp	Val	Lys	Asn	Gln	Gly	Asn	Asn		
			125						130					

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<213> *Ehrlichia canis*

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<223> amino acid sequence of p28-4 protien

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			20						25					30
Ser	Thr	Ile	His	Asn	Phe	Tyr	Ile	Ser	Gly	Lys	Tyr	Met	Pro	Thr
			35						40					45
Ala	Ser	His	Phe	Gly	Ile	Phe	Ser	Ala	Lys	Glu	Glu	Gln	Ser	Phe
			50						55					60
Thr	Lys	Val	Leu	Val	Gly	Leu	Asp	Gln	Arg	Leu	Ser	His	Asn	Ile
			65						70					75
Ile	Asn	Asn	Asn	Asp	Thr	Ala	Lys	Ser	Leu	Lys	Val	Gln	Asn	Tyr
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Ser	Phe	Lys	Tyr	Lys	Asn	Asn	Pro	Phe	Leu	Gly	Phe	Ala	Gly	Ala
			95						100					105
Ile	Gly	Tyr	Ser	Ile	Gly	Asn	Ser	Arg	Ile	Glu	Leu	Glu	Val	Ser
			110						115					120
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Ala	Ser	His	Phe	Gly	Val	Phe	Ser	Ala	Lys	Glu	Glu	Arg	Asn	Thr	50	55	60
Thr	Val	Gly	Val	Phe	Gly	Leu	Lys	Gln	Asn	Trp	Asp	Gly	Ser	Ala	65	70	75
Ile	Ser	Asn	Ser	Ser	Pro	Asn	Asp	Val	Phe	Thr	Val	Ser	Asn	Tyr	80	85	90
Ser	Phe	Lys	Tyr	Glu	Asn	Asn	Pro	Phe	Leu	Gly	Phe	Ala	Gly	Ala	95	100	105
Ile	Gly	Tyr	Ser	Met	Asp	Gly	Pro	Arg	Ile	Glu	Leu	Glu	Val	Ser	110	115	120
Tyr	Glu	Thr	Phe	Asp	Val	Lys	Asn	Gln	Gly	Asn	Asn	Tyr	Lys	Asn	125	130	135
Glu	Ala	His	Arg	Tyr	Cys	Ala	Leu	Ser	His	Asn	Ser	Ala	Ala	Asp	140	145	150
Met	Ser	Ser	Ala	Ser	Asn	Asn	Phe	Val	Phe	Leu	Lys	Asn	Glu	Gly	155	160	165
Leu	Leu	Asp	Ile	Ser	Phe	Met	Leu	Asn	Ala	Cys	Tyr	Asp	Val	Val	170	175	180
Gly	Glu	Gly	Ile	Pro	Phe	Ser	Pro	Tyr	Ile	Cys	Ala	Gly	Ile	Gly	185	190	195
Thr	Asp	Leu	Val	Ser	Met	Phe	Glu	Ala	Thr	Asn	Pro	Lys	Ile	Ser	200	205	210
Tyr	Gln	Gly	Lys	Leu	Gly	Leu	Ser	Tyr	Ser	Ile	Ser	Pro	Glu	Ala	215	220	225
Ser	Val	Phe	Ile	Gly	Gly	His	Phe	His	Lys	Val	Ile	Gly	Asn	Glu	230	235	240
Phe	Arg	Asp	Ile	Pro	Thr	Ile	Ile	Pro	Thr	Gly	Ser	Thr	Leu	Ala	245	250	255
Gly	Lys	Gly	Asn	Tyr	Pro	Ala	Ile	Val	Ile	Leu	Asp	Val	Cys	His	260	265	270

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<213> *Ehrlichia chaffeensis*

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<223> amino acid sequence of *E. chaffeensis* OMP-1B

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35	40 45
Val Lys Tyr Asn Pro Ser Ile Ser His Phe Arg Lys Phe Ser Ala	
50	55 60
Glu Glu Ala Pro Ile Asn Gly Asn Thr Ser Ile Thr Lys Lys Val	
65	70 75
Phe Gly Leu Lys Lys Asp Gly Asp Ile Ala Gln Ser Ala Asn Phe	
80	85 90
Asn Arg Thr Asp Pro Ala Leu Glu Phe Gln Asn Asn Leu Ile Ser	
95	100 105
Gly Phe Ser Gly Ser Ile Gly Tyr Ala Met Asp Gly Pro Arg Ile	
110	115 120
Glu Leu Glu Ala Ala Tyr Gln Lys Phe Asp Ala Lys Asn Pro Asp	
125	130 135
Asn Asn Asp Thr Asn Ser Gly Asp Tyr Tyr Lys Tyr Phe Gly Leu	
140	145 150
Ser Arg Glu Asp Ala Ile Ala Asp Lys Lys Tyr Val Val Leu Lys	
155	160 165

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Asp	Ile	Thr	Ala	Glu	Gly	Val	Pro	Phe	Ile	Pro	Tyr	Ala	Cys	Ala
				185					190					195
Gly	Val	Gly	Ala	Asp	Leu	Ile	Asn	Val	Phe	Lys	Asp	Phe	Asn	Leu
				200					205					210
Lys	Phe	Ser	Tyr	Gln	Gly	Lys	Ile	Gly	Ile	Ser	Tyr	Pro	Ile	Thr
				215					220					225
Pro	Glu	Val	Ser	Ala	Phe	Ile	Gly	Gly	Tyr	Tyr	His	Gly	Val	Ile
				230					235					240
Gly	Asn	Asn	Phe	Asn	Lys	Ile	Pro	Val	Ile	Thr	Pro	Val	Val	Leu
				245					250					255
Glu	Gly	Ala	Pro	Gln	Thr	Thr	Ser	Ala	Leu	Val	Thr	Ile	Asp	Thr
				260					265					270
Gly	Tyr	Phe	Gly	Gly	Glu	Val	Gly	Val	Arg	Phe	Thr	Phe		
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<212> PRT

<213> *Ehrlichia chaffeensis*

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<223> amino acid sequence of *E. chaffeensis* OMP-1C

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Asp	Ser	Val	Ser	Gly	Asn	Phe	Tyr	Ile	Ser	Gly	Lys	Tyr	Met	Pro
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Ser	Ala	Ser	His	Phe	Gly	Val	Phe	Ser	Ala	Lys	Glu	Glu	Lys	Asn
				50					55					60

Pro	Thr	Val	Ala	Leu	Tyr	Gly	Leu	Lys	Gln	Asp	Trp	Asn	Gly	Val	
				65					70					75	
Ser	Ala	Ser	Ser	His	Ala	Asp	Ala	Asp	Phe	Asn	Asn	Lys	Gly	Tyr	
				80					85					90	
Ser	Phe	Lys	Tyr	Glu	Asn	Asn	Pro	Phe	Leu	Gly	Phe	Ala	Gly	Ala	
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Ile	Gly	Tyr	Ser	Met	Gly	Gly	Pro	Arg	Ile	Glu	Phe	Glu	Val	Ser	
				110					115					120	
Tyr	Glu	Thr	Phe	Asp	Val	Lys	Asn	Gln	Gly	Gly	Asn	Tyr	Lys	Asn	
				125					130					135	
Asp	Ala	His	Arg	Tyr	Cys	Ala	Leu	Asp	Arg	Lys	Ala	Ser	Ser	Thr	
				140					145					150	
Asn	Ala	Thr	Ala	Ser	His	Tyr	Val	Leu	Leu	Lys	Asn	Glu	Gly	Leu	
				155					160					165	
Leu	Asp	Ile	Ser	Leu	Met	Leu	Asn	Ala	Cys	Tyr	Asp	Val	Val	Ser	
				170					175					180	
Glu	Gly	Ile	Pro	Phe	Ser	Pro	Tyr	Ile	Cys	Ala	Gly	Val	Gly	Thr	
				185					190					195	
Asp	Leu	Ile	Ser	Met	Phe	Glu	Ala	Ile	Asn	Pro	Lys	Ile	Ser	Tyr	
				200					205					210	
Gln	Gly	Lys	Leu	Gly	Leu	Ser	Tyr	Ser	Ile	Asn	Pro	Glu	Ala	Ser	
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Val	Phe	Val	Gly	Gly	His	Phe	His	Lys	Val	Ala	Gly	Asn	Glu	Phe	
				230					235					240	
Arg	Asp	Ile	Ser	Thr	Leu	Lys	Ala	Phe	Ala	Thr	Pro	Ser	Ser	Ala	
				245					250					255	
Ala	Thr	Pro	Asp	Leu	Ala	Thr	Val	Thr	Leu	Ser	Val	Cys	His	Phe	
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Gly	Val	Glu	Leu	Gly	Gly	Arg	Phe	Asn	Phe						
				275					280						

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<213> *Ehrlichia chaffeensis*

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<223> amino acid sequence of *E. chaffeensis* OMP-1D

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Asp	Asn	Ile	Ser	Gly	Asn	Phe	Tyr	Ile	Ser	Gly	Lys	Tyr	Met	Pro
				35					40				45	
Ser	Ala	Ser	His	Phe	Gly	Val	Phe	Ser	Ala	Lys	Glu	Glu	Arg	Asn
				50					55				60	
Thr	Thr	Val	Gly	Val	Phe	Gly	Ile	Glu	Gln	Asp	Trp	Asp	Arg	Cys
				65					70				75	
Val	Ile	Ser	Arg	Thr	Thr	Leu	Ser	Asp	Ile	Phe	Thr	Val	Pro	Asn
				80					85				90	
Tyr	Ser	Phe	Lys	Tyr	Glu	Asn	Asn	Leu	Phe	Ser	Gly	Phe	Ala	Gly
				95					100				105	
Ala	Ile	Gly	Tyr	Ser	Met	Asp	Gly	Pro	Arg	Ile	Glu	Leu	Glu	Val
				110					115				120	
Ser	Tyr	Glu	Ala	Phe	Asp	Val	Lys	Asn	Gln	Gly	Asn	Asn	Tyr	Lys
				125					130				135	
Asn	Glu	Ala	His	Arg	Tyr	Tyr	Ala	Leu	Ser	His	Leu	Leu	Gly	Thr
				140					145				150	
Glu	Thr	Gln	Ile	Asp	Gly	Ala	Gly	Ser	Ala	Ser	Val	Phe	Leu	Ile
				155					160				165	
Asn	Glu	Gly	Leu	Leu	Asp	Lys	Ser	Phe	Met	Leu	Asn	Ala	Cys	Tyr
				170					175				180	
Asp	Val	Ile	Ser	Glu	Gly	Ile	Pro	Phe	Ser	Pro	Tyr	Ile	Cys	Ala
				185					190				195	
Gly	Ile	Gly	Ile	Asp	Leu	Val	Ser	Met	Phe	Glu	Ala	Ile	Asn	Pro
				200					205				210	

Lys	Ile	Ser	Tyr	Gln	Gly	Lys	Leu	Gly	Leu	Ser	Tyr	Pro	Ile	Ser
				215					220					225
Pro	Glu	Ala	Ser	Val	Phe	Ile	Gly	Gly	His	Phe	His	Lys	Val	Ile
				230					235					240
Gly	Asn	Glu	Phe	Arg	Asp	Ile	Pro	Thr	Met	Ile	Pro	Ser	Glu	Ser
				245					250					255
Ala	Leu	Ala	Gly	Lys	Gly	Asn	Tyr	Pro	Ala	Ile	Val	Thr	Leu	Asp
				260					265					270
Val	Phe	Tyr	Phe	Gly	Ile	Glu	Leu	Gly	Gly	Arg	Phe	Asn	Phe	Gln
				275					280					285

Leu

<210> 13
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 <223> amino acid sequence of *E. chaffeensis* OMP-1E

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 20 25 30
 Asp Asn Ile Ser Gly Asn Phe Tyr Val Ser Gly Lys Tyr Met Pro
 35 40 45
 Ser Ala Ser His Phe Gly Met Phe Ser Ala Lys Glu Glu Lys Asn
 50 55 60
 Pro Thr Val Ala Leu Tyr Gly Leu Lys Gln Asp Trp Glu Gly Ile
 65 70 75
 Ser Ser Ser Ser His Asn Asp Asn His Phe Asn Asn Lys Gly Tyr
 80 85 90
 Ser Phe Lys Tyr Glu Asn Asn Pro Phe Leu Gly Phe Ala Gly Ala
 95 100 105

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Ile	Gly	Tyr	Ser	Met	Gly	Gly	Pro	Arg	Val	Glu	Phe	Glu	Val	Ser
				110					115					120
Tyr	Glu	Thr	Phe	Asp	Val	Lys	Asn	Gln	Gly	Asn	Asn	Tyr	Lys	Asn
				125					130					135
Asp	Ala	His	Arg	Tyr	Cys	Ala	Leu	Gly	Gln	Gln	Asp	Asn	Ser	Gly
				140					145					150
Ile	Pro	Lys	Thr	Ser	Lys	Tyr	Val	Leu	Leu	Lys	Ser	Glu	Gly	Leu
				155					160					165
Leu	Asp	Ile	Ser	Phe	Met	Leu	Asn	Ala	Cys	Tyr	Asp	Ile	Ile	Asn
				170					175					180
Glu	Ser	Ile	Pro	Leu	Ser	Pro	Tyr	Ile	Cys	Ala	Gly	Val	Gly	Thr
				185					190					195
Asp	Leu	Ile	Ser	Met	Phe	Glu	Ala	Thr	Asn	Pro	Lys	Ile	Ser	Tyr
				200					205					210
Gln	Gly	Lys	Leu	Gly	Leu	Ser	Tyr	Ser	Ile	Asn	Pro	Glu	Ala	Ser
				215					220					225
Val	Phe	Ile	Gly	Gly	His	Phe	His	Lys	Val	Ile	Gly	Asn	Glu	Phe
				230					235					240
Arg	Asp	Ile	Pro	Thr	Leu	Lys	Ala	Phe	Val	Thr	Ser	Ser	Ala	Thr
				245					250					255
Pro	Asp	Leu	Ala	Ile	Val	Thr	Leu	Ser	Val	Cys	His	Phe	Gly	Ile
				260					265					270
Glu	Leu	Gly	Gly	Arg	Phe	Asn	Phe							
				275										

<210> 14
 <211> 280
 <212> PRT
 <213> *Ehrlichia chaffeensis*

 <220>
 <223> amino acid sequence of *E. chaffeensis* OMP-1F

<400>														14	
Met	Asn	Cys	Lys	Lys	Phe	Phe	Ile	Thr	Thr	Thr	Leu	Val	Ser	Leu	
				5							10				15
Met	Ser	Phe	Leu	Pro	Gly	Ile	Ser	Phe	Ser	Asp	Ala	Val	Gln	Asn	
				20							25				30
Asp	Asn	Val	Gly	Gly	Asn	Phe	Tyr	Ile	Ser	Gly	Lys	Tyr	Val	Pro	
				35							40				45
Ser	Val	Ser	His	Phe	Gly	Val	Phe	Ser	Ala	Lys	Gln	Glu	Arg	Asn	
				50							55				60
Thr	Thr	Thr	Gly	Val	Phe	Gly	Leu	Lys	Gln	Asp	Trp	Asp	Gly	Ser	
				65							70				75
Thr	Ile	Ser	Lys	Asn	Ser	Pro	Glu	Asn	Thr	Phe	Asn	Val	Pro	Asn	
				80							85				90
Tyr	Ser	Phe	Lys	Tyr	Glu	Asn	Asn	Pro	Phe	Leu	Gly	Phe	Ala	Gly	
				95							100				105
Ala	Val	Gly	Tyr	Leu	Met	Asn	Gly	Pro	Arg	Ile	Glu	Leu	Glu	Met	
				110							115				120
Ser	Tyr	Glu	Thr	Phe	Asp	Val	Lys	Asn	Gln	Gly	Asn	Asn	Tyr	Lys	
				125							130				135
Asn	Asp	Ala	His	Lys	Tyr	Tyr	Ala	Leu	Thr	His	Asn	Ser	Gly	Gly	
				140							145				150
Lys	Leu	Ser	Asn	Ala	Gly	Asp	Lys	Phe	Val	Phe	Leu	Lys	Asn	Glu	
				155							160				165
Gly	Leu	Leu	Asp	Ile	Ser	Leu	Met	Leu	Asn	Ala	Cys	Tyr	Asp	Val	
				170							175				180
Ile	Ser	Glu	Gly	Ile	Pro	Phe	Ser	Pro	Tyr	Ile	Cys	Ala	Gly	Val	
				185							190				195
Gly	Thr	Asp	Leu	Ile	Ser	Met	Phe	Glu	Ala	Ile	Asn	Pro	Lys	Ile	
				200							205				210
Ser	Tyr	Gln	Gly	Lys	Leu	Gly	Leu	Ser	Tyr	Ser	Ile	Ser	Pro	Glu	
				215							220				225
Ala	Ser	Val	Phe	Val	Gly	Gly	His	Phe	His	Lys	Val	Ile	Gly	Asn	
				230							235				240
Glu	Phe	Arg	Asp	Ile	Pro	Ala	Met	Ile	Pro	Ser	Thr	Ser	Thr	Leu	
				245							250				255

Thr	Gly	Asn	His	Phe	Thr	Ile	Val	Thr	Leu	Ser	Val	Cys	His	Phe
				260					265					270

Gly	Val	Glu	Leu	Gly	Gly	Arg	Phe	Asn	Phe
				275					280

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<211> 284

<212> PRT

<213> *Cowdria ruminantium*

<220>

<223> amino acid sequence of *C. ruminantium* MAP-1

<400> 15

Met	Asn	Cys	Lys	Lys	Ile	Phe	Ile	Thr	Ser	Thr	Leu	Ile	Ser	Leu
				5					10					15
Val	Ser	Phe	Leu	Pro	Gly	Val	Ser	Phe	Ser	Asp	Val	Ile	Gln	Glu
				20					25					30
Glu	Asn	Asn	Pro	Val	Gly	Ser	Val	Tyr	Ile	Ser	Ala	Lys	Tyr	Met
				35					40					45
Pro	Thr	Ala	Ser	His	Phe	Gly	Lys	Met	Ser	Ile	Lys	Glu	Asp	Ser
				50					55					60
Arg	Asp	Thr	Lys	Ala	Val	Phe	Gly	Leu	Lys	Lys	Asp	Trp	Asp	Gly
				65					70					75
Val	Lys	Thr	Pro	Ser	Gly	Asn	Thr	Asn	Ser	Ile	Phe	Thr	Glu	Lys
				80					85					90
Asp	Tyr	Ser	Phe	Lys	Tyr	Glu	Asn	Asn	Pro	Phe	Leu	Gly	Phe	Ala
				95					100					105
Gly	Ala	Val	Gly	Tyr	Ser	Met	Asn	Gly	Pro	Arg	Ile	Glu	Phe	Glu
				110					115					120
Val	Ser	Tyr	Glu	Thr	Phe	Asp	Val	Arg	Asn	Pro	Gly	Gly	Asn	Tyr
				125					130					135
Lys	Asn	Asp	Ala	His	Met	Tyr	Cys	Ala	Leu	Asp	Thr	Ala	Ser	Ser
				140					145					150

Ser Thr Ala Gly Ala Thr Thr Ser Val Met Val Lys Asn Glu Asn		
	155	160
Leu Thr Asp Ile Ser Leu Met Leu Asn Ala Cys Tyr Asp Ile Met		
	170	175
Leu Asp Gly Met Pro Val Ser Pro Tyr Val Cys Ala Gly Ile Gly		
	185	190
Thr Asp Leu Val Ser Val Ile Asn Ala Thr Asn Pro Lys Leu Ser		
	200	205
Tyr Gln Gly Lys Leu Gly Ile Ser Tyr Ser Ile Asn Pro Glu Ala		
	215	220
Ser Ile Phe Ile Gly Gly His Phe His Arg Val Ile Gly Asn Glu		
	230	235
Phe Lys Asp Ile Ala Thr Ser Lys Val Phe Thr Ser Ser Gly Asn		
	245	250
Ala Ser Ser Ala Val Ser Pro Gly Phe Ala Ser Ala Ile Leu Asp		
	260	265
Val Cys His Phe Gly Ile Glu Ile Gly Gly Arg Phe Val Phe		
	275	280

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 <213> artificial sequence

<220>
 <221> primer_bind
 <222> nucleotides 313-332 of *C. ruminantium* MAP-1,
 also nucleotides 307-326 of *E. chaffeensis* P28
 <223> forward primer 793 for PCR

<400> 16

gcaggagctg ttggttactc 20

<210> 17
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 <212> DNA
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 <220>
 <221> primer_bind
 <222> nucleotides 823-843 of *C. ruminantium* MAP-1,
 also nucleotides 814-834 of *E. chaffeensis* P28
 <223> reverse primer 1330 for PCR

<400> 17

ccttcctcca agttctatgc c

21

<210> 18
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 <212> DNA
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<220>

<221> primer_bind

<223> primer 46f, specific for p28-5 gene

<400> 18

atatacttcc tacctaattgt ctca

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<221> primer_bind

<223> primer used for sequencing 28-kDa protein
genes in *E. canis*

<400> 19
agtgcagagt cttcggtttc 20

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<223> primer used for sequencing 28-kDa protein
genes in *E. canis*

<400> 20
gttacttgcg gaggacat 18

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<221> primer_bind
<222> nucleotides 687-710 of *E. canis* p28-7
<223> primer 394 for PCR

<400> 21
gcatttccac aggatcatag gtaa 24

<210> 22
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 <212> DNA
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 <222> nucleotides 710-687 of *E. canis* p28-7
 <223> primer 394C for PCR

<400> 22
 ttacctatga tcctgtggaa atgc 24

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 <220>
 <221> primer_bind
 <223> primer 793C which anneals to a region with *E. canis*
 p28-7, used to amplify the intergenic region
 between gene p28-6 and p28-7

<400> 23
 gagtaaccaa cagctcctgc 20

<210> 24
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 <212> DNA
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 <220>
 <221> primer_bind

<222>

<223> primer EC28OM-F complementary to noncoding regions
adjacent to the open reading frame of *p28-7*

<400> 24

tctacttttgc acttccacta ttgt 24

<210> 25

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<212> DNA

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<220>

<221> primer_bind

<222>

<223> primer EC28OM-R complementary to noncoding regions
adjacent to the open reading frame of *p28-7*

<400> 25

attctttttgc cactatttttt cttt 24

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<220>

<221> primer_bind

<223> primer *ECaSA3-2* corresponding to regions within
p28-6, used to amplify the intergenic region NC3
between gene *p28-6* and *p28-7*

<400> 26

ctaggattag gttatagtat aagtt 25

<210> 27
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 <213> *Ehrlichia canis*

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 <221> PEPTIDE
 <223> a predicted N-terminal signal peptide of p28-7
 and p28-6

<400> 27

Met Asn Cys Lys Lys Ile Leu Ile Thr Thr Ala Leu Met Ser Leu

5 10 15

Met Tyr Tyr Ala Pro Ser Ile Ser

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 <213> *Ehrlichia chaffeensis*

<220>

<223> amino acid sequence of N-terminal signal peptide of
E. chaffeensis P28

<400> 28

Met Asn Tyr Lys Lys Ile Leu Ile Thr Ser Ala Leu Ile Ser Leu

5 10 15

Ile Ser Ser Leu Pro Gly Val Ser Phe Ser

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<210> 29

<211> 26

<212> PRT
 <213> *Ehrlichia canis*

<220>
 <223> amino acid sequence of putative cleavage site of
 p28-7

<400> 29
 Met Asn Cys Lys Lys Ile Leu Ile Thr Thr Ala Leu Ile Ser Leu
 5 10 15
 Met Tyr Ser Ile Pro Ser Ile Ser Ser Phe Ser
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<210> 30
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 <212> DNA
 <213> *Ehrlichia canis*

<220>
 <223> nucleic acid sequence of intergenic
 noncoding region 1 (28NC1)

<400> 30
 taatacttct attgtacatg ttaaaaatag tactagtttg cttctgtggt 50
 ttataaacgc aagagagaaa tagttagtaa taaattagaa agttaaatat 100
 tagaaaagtc atatgttttt cattgtcatt gatactcaac taaaagtagt 150
 ataaatgtta cttattaata attttacgta gtatattaaa tttcccttac 200
 aaaagccact agtattttat actaaaagct atactttggc ttgtatttaa 250
 tttgtatttt tactactggt aatttacttt cactgtttct ggtgtaaat 299

<210> 31
 <211> 345
 <212> DNA
 <213> *Ehrlichia canis*

<220>

<223> nucleic acid sequence of intergenic noncoding
region 2 (28NC2)

<400> 31

taatttcgtg gtacacatat cacgaagcta aaattgtttt tttatctctg 50
ctgtatacaa gagaaaaaat agtagtgaaa attacctaac aatatgacag 100
tacaagttta ccaagcttat tctcacaaaa cttcttgtgt cttttatctc 150
tttacaatga aatgtacact tagcttcact actgtagagt gtgtttatca 200
atgctttgtt tattaatact ctacataata tgttaaattt ttcttacaaa 250
actcactagt aatttatact agaatatata ttctgacttg tatttgcttt 300
atacttccac tattgttaat ttattttcac tatttttaggt gtaat 345

<210> 32

<211> 345

<212> DNA

<213> *Ehrlichia canis*

<220>

<223> nucleic acid sequence of intergenic
noncoding region 3 (28NC3)

<400> 32

tgattttatt gttgccacat attaaaaatg atctaaactt gtttttatta 50
ttgctacata caaaaaaaag aaaaatagtg gcaaaagaat gtagcaataa 100
gagggggggg ggggactaaa tttaccttct attcttctaa tattctttac 150
tatattcaaa tagcacaact caatgcttcc aggaaaatat gtttctaata 200
ttttatttat taccaatcct tatataatat attaaatttc tcttacaaaa 250
atctctaagt ttttatactt aatatatata ttctggcttg tatttacttt 300
gcacttccac tattgttaat ttattttcac tatttttaggt gtaat 345

<210> 33

<211> 355

<212> DNA

<213> *Ehrlichia canis*

<220>

<223> nucleic acid sequence of intergenic
noncoding region 4 (28NC4)

<400> 33

taattttatt gttgccacat attaaaaatg atctaaactt gtttttawta 50
ttgctacata caaaaaaaga aaaatagtgg caaaagaatg tagcaataag 100
agggggggggg gggaccaaatt ttatcttcta tgcttcccaa gttttttcyc 150
gctattttatg acttaaaciaa cagaaggtaa `tatcctcacg gaaaacttat 200
cttcaaatat tttattttatt accaatctta tataatatat taaattttctc 250
ttacaaaaat cactagtatt ttatacaaaa atatatatc tgacttgctt 300
ttcttctgca cttctactat ttttaattta tttgtcacta ttaggttata 350
ataaw 355

<210> 34

<211> 24

<212> DNA

<213> artificial sequence

<220>

<223> primer p28-5-818f

<400> 34

ttaaacatat gccacttcgg acta 24

<210> 35

<211> 28

<212> DNA

<213> artificial sequence

<220>

<223> primer 1191

<400> 35
tatgatcgtg taaaattgct gtgagtat 28

<210> 36

<211> 20

<212> DNA

<213> artificial sequence

<220>

<223> primer ECa28-75C

<400> 36
tactggcagc tgctggacta 20

<210> 37

<211> 22

<212> DNA

<213> artificial sequence

<220>

<223> primer ECa5'-1600

<400> 37
caccaataaa tgcagagact tc 22

<210> 38

<211> 26

<212> DNA

<213> artificial sequence

<220>

<223> primer 3125

<400> 38
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<210> 39

<211> 879

<212> DNA

<213> *Ehrlichia canis*

<220>

<223> nucleic acid sequence of *E. canis* p28-1

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gttttccagta attttttcagt taaagaaacc aatgtcataa ctaaaaacct 200
tatagcttta aaaaaagatg ttgactctat tgaaaccaag actgatgcca 250
gtgtaggtat tagtaaccca tcaaatttta ctatccccta tacagctgta 300
tttcaagata attctgtcaa tttcaatgga actattgggtt acacctttgc 350
tgaaggtaca agagttgaaa tagaagggttc ttatgaggaa tttgatgtta 400
aaaaccctgg aggctataca ctaagtgatg cctatcgcta ttttgcatta 450
gcacgtgaaa tgaaaggtaa tagttttaca cctaaagaaa aagtttctaa 500
tagtatTTTT cactctgtaa tgagaaatga tggattatct ataatatctg 550
ttatagtaaa tgtttgcctac gattttctctt tgaacaattt gtcaatatcg 600
ccttacatat gtggaggagc aggggtagat gctatagaat tcttcgatgt 650
attacacatt aagtttgcct atcaaagcaa gctaggtatt gcttattctc 700
taccatctaa cattagtctc tttgctagtt tatattacca taaagtaatg 750
ggcaatcaat ttaaaaattt aaatgtccaa catgttgctg aacttgcaag 800
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gaggtgaaat tgggtgcaaga ttgacattt 879

<210> 40

<211> 293

<212> PRT

<213> *Ehrlichia canis*

<220>

<223> amino acid sequence of *E. canis* p28-1 protein

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Cys	Leu	Leu	Ser	Leu	Pro	Asn	Ile	Ser	Ser	Ser	Lys	Ala	Ile	Asn
			20						25				30	
Asn	Asn	Ala	Lys	Lys	Tyr	Tyr	Gly	Leu	Tyr	Ile	Ser	Gly	Gln	Tyr
			35						40				45	
Lys	Pro	Ser	Val	Ser	Val	Phe	Ser	Asn	Phe	Ser	Val	Lys	Glu	Thr
			50						55				60	
Asn	Val	Ile	Thr	Lys	Asn	Leu	Ile	Ala	Leu	Lys	Lys	Asp	Val	Asp
			65						70				75	
Ser	Ile	Glu	Thr	Lys	Thr	Asp	Ala	Ser	Val	Gly	Ile	Ser	Asn	Pro
			80						85				90	
Ser	Asn	Phe	Thr	Ile	Pro	Tyr	Thr	Ala	Val	Phe	Gln	Asp	Asn	Ser
			95						100				105	
Val	Asn	Phe	Asn	Gly	Thr	Ile	Gly	Tyr	Thr	Phe	Ala	Glu	Gly	Thr
			110						115				120	
Arg	Val	Glu	Ile	Glu	Gly	Ser	Tyr	Glu	Glu	Phe	Asp	Val	Lys	Asn
			125						130				135	
Pro	Gly	Gly	Tyr	Thr	Leu	Ser	Asp	Ala	Tyr	Arg	Tyr	Phe	Ala	Leu
			140						145				150	
Ala	Arg	Glu	Met	Lys	Gly	Asn	Ser	Phe	Thr	Pro	Lys	Glu	Lys	Val
			155						160				165	
Ser	Asn	Ser	Ile	Phe	His	Thr	Val	Met	Arg	Asn	Asp	Gly	Leu	Ser
			170						175				180	
Ile	Ile	Ser	Val	Ile	Val	Asn	Val	Cys	Tyr	Asp	Phe	Ser	Leu	Asn
			185						190				195	
Asn	Leu	Ser	Ile	Ser	Pro	Tyr	Ile	Cys	Gly	Gly	Ala	Gly	Val	Asp
			200						205				210	
Ala	Ile	Glu	Phe	Phe	Asp	Val	Leu	His	Ile	Lys	Phe	Ala	Tyr	Gln
			215						220				225	
Ser	Lys	Leu	Gly	Ile	Ala	Tyr	Ser	Leu	Pro	Ser	Asn	Ile	Ser	Leu
			230						235				240	

Phe	Ala	Ser	Leu	Tyr	Tyr	His	Lys	Val	Met	Gly	Asn	Gln	Phe	Lys
				245					250					255
Asn	Leu	Asn	Val	Gln	His	Val	Ala	Glu	Leu	Ala	Ser	Ile	Pro	Lys
				260					265					270
Ile	Thr	Ser	Ala	Val	Ala	Thr	Leu	Asn	Ile	Gly	Tyr	Phe	Gly	Gly
				275					280					285
Glu	Ile	Gly	Ala	Arg	Leu	Thr	Phe							
				290			293							

<210> 41

<211> 840

<212> DNA

<213> *Ehrlichia canis*

<220>

<223> nucleic acid sequence of *E. canis* p28-2

<400> 41

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ataacaaaga	aggcttctac	attagtgcaa	agtacaatcc	aagtatatca	150
cactttagaa	aattctctgc	tgaagaaact	cctattaatg	gaacaaattc	200
tctcactaaa	aaagttttcg	gactaaagaa	agatggtgat	ataacaaaaa	250
aagacgattt	tacaagagta	gctccaggca	ttgattttca	aaataactta	300
atatcaggat	tttcaggaag	tattgggttac	tctatggacg	gaccaagaat	350
agaacttgaa	gctgcatatc	aacaatttaa	tccaaaaaac	accgataaca	400
atgatactga	taatggtgaa	tactataaac	atcttgcatc	atctcgtaaa	450
gatgcaatgg	aagatcagca	atatgtagta	cttaaaaatg	acggcataac	500
ttttatgtca	ttgatggtta	atacttgcta	tgacattaca	gctgaaggag	550
tatctttcgt	accatatgca	tgtgcaggta	taggagcaga	tcttatcact	600
atcttttaag	acctcaatct	aaaatttgct	taccaaggaa	aaataggtat	650
tagttaccct	atcacaccag	aagtctctgc	atcttattgg	ggatactacc	700
atggcgttat	tggttaataa	tttgagaaga	tacctgtaat	aactcctgta	750
gtattaaatg	atgctcctca	aaccacatct	gcttcagtaa	ctcttgacgt	800
tggatacttt	ggcggagaaa	ttggaatgag	gttcaccttc		840

<210> 42
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 <212> PRT
 <213> *Ehrlichia canis*

 <220>
 <223> amino acid sequence of *E. canis* p28-2 protein

<400> 42
 Met Asn Tyr Lys Lys Ile Leu Val Arg Ser Ala Leu Ile Ser Leu
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 Met Ser Ile Leu Pro Tyr Gln Ser Phe Ala Asp Pro Val Gly Ser
 20 25 30
 Arg Thr Asn Asp Asn Lys Glu Gly Phe Tyr Ile Ser Ala Lys Tyr
 35 40 45
 Asn Pro Ser Ile Ser His Phe Arg Lys Phe Ser Ala Glu Glu Thr
 50 55 60
 Pro Ile Asn Gly Thr Asn Ser Leu Thr Lys Lys Val Phe Gly Leu
 65 70 75
 Lys Lys Asp Gly Asp Ile Thr Lys Lys Asp Asp Phe Thr Arg Val
 80 85 90
 Ala Pro Gly Ile Asp Phe Gln Asn Asn Leu Ile Ser Gly Phe Ser
 95 100 105
 Gly Ser Ile Gly Tyr Ser Met Asp Gly Pro Arg Ile Glu Leu Glu
 110 115 120
 Ala Ala Tyr Gln Gln Phe Asn Pro Lys Asn Thr Asp Asn Asn Asp
 125 130 135
 Thr Asp Asn Gly Glu Tyr Tyr Lys His Phe Ala Leu Ser Arg Lys
 140 145 150
 Asp Ala Met Glu Asp Gln Gln Tyr Val Val Leu Lys Asn Asp Gly
 155 160 165
 Ile Thr Phe Met Ser Leu Met Val Asn Thr Cys Tyr Asp Ile Thr
 170 175 180
 Ala Glu Gly Val Ser Phe Val Pro Tyr Ala Cys Ala Gly Ile Gly
 185 190 195

Ala Asp Leu Ile Thr Ile Phe Lys Asp Leu Asn Leu Lys Phe Ala		
	200	205 210
Tyr Gln Gly Lys Ile Gly Ile Ser Tyr Pro Ile Thr Pro Glu Val		
	215	220 225
Ser Ala Phe Ile Gly Gly Tyr Tyr His Gly Val Ile Gly Asn Lys		
	230	235 240
Phe Glu Lys Ile Pro Val Ile Thr Pro Val Val Leu Asn Asp Ala		
	245	250 255
Pro Gln Thr Thr Ser Ala Ser Val Thr Leu Asp Val Gly Tyr Phe		
	260	265 270
Gly Gly Glu Ile Gly Met Arg Phe Thr Phe		
	275	280

<210> 43

<211> 828

<212> DNA

<213> *Ehrlichia canis*

<220>

<223> nucleic acid sequence of *E. canis* p28-3

<400> 43

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gggaactttt cagctaaaga agaaaaaaac acaacaactg gaattttttgg 200
attaaaagaa tcatggactg gtggtatcat ccttgataaa gaacatgcag 250
cttttaatat cccaaattat tcattttaa atgaaaataa tccatttttta 300
ggatttgcag gggtaattgg ctattcaata ggtagtccaa gaatagaatt 350
tgaagtatca tacgagacat tcgatgtaca aaatccagga gataagttta 400
acaatgatgc acataagtat tgtgctttat ccaatgattc cagtaaaaca 450
atgaaaagtg gtaaattcgt ttttctcaa aatgaaggat taagtgacat 500
atcactcatg ttaaattgtat gttatgatat aataaacaaa agaatgcctt 550
tttcacctta catatgtgca ggcattggta ctgacttaat attcatgttt 600
gacgctataa accataaagc tgcttatcaa ggaaaattag gttttaatta 650

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tccaataagc ccagaagcta acatttctat ggggtgtgcac tttcacaaag 700
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 gttagaattt gggtacaggg tcagtttt 828

<210> 44

<211> 276

<212> PRT

<213> *Ehrlichia canis* .

<220>

<223> amino acid sequence of *E. canis* p28-3 protein

<400> 44

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Thr	Ile	Leu	Leu	Pro	Gly	Ile	Ser	Phe	Ser	Lys	Pro	Ile	His	Glu
			20						25					30
Asn	Asn	Thr	Thr	Gly	Asn	Phe	Tyr	Ile	Ile	Gly	Lys	Tyr	Val	Pro
			35						40					45
Ser	Ile	Ser	His	Phe	Gly	Asn	Phe	Ser	Ala	Lys	Glu	Glu	Lys	Asn
			50						55					60
Thr	Thr	Thr	Gly	Ile	Phe	Gly	Leu	Lys	Glu	Ser	Trp	Thr	Gly	Gly
			65						70					75
Ile	Ile	Leu	Asp	Lys	Glu	His	Ala	Ala	Phe	Asn	Ile	Pro	Asn	Tyr
			80						85					90
Ser	Phe	Lys	Tyr	Glu	Asn	Asn	Pro	Phe	Leu	Gly	Phe	Ala	Gly	Val
			95						100					105
Ile	Gly	Tyr	Ser	Ile	Gly	Ser	Pro	Arg	Ile	Glu	Phe	Glu	Val	Ser
			110						115					120
Tyr	Glu	Thr	Phe	Asp	Val	Gln	Asn	Pro	Gly	Asp	Lys	Phe	Asn	Asn
			125						130					135
Asp	Ala	His	Lys	Tyr	Cys	Ala	Leu	Ser	Asn	Asp	Ser	Ser	Lys	Thr
			140						145					150

Met	Lys	Ser	Gly	Lys	Phe	Val	Phe	Leu	Lys	Asn	Glu	Gly	Leu	Ser
				155					160					165
Asp	Ile	Ser	Leu	Met	Leu	Asn	Val	Cys	Tyr	Asp	Ile	Ile	Asn	Lys
				170					175					180
Arg	Met	Pro	Phe	Ser	Pro	Tyr	Ile	Cys	Ala	Gly	Ile	Gly	Thr	Asp
				185					190					195
Leu	Ile	Phe	Met	Phe	Asp	Ala	Ile	Asn	His	Lys	Ala	Ala	Tyr	Gln
				200					205					210
Gly	Lys	Leu	Gly	Phe	Asn	Tyr	Pro	Ile	Ser	Pro	Glu	Ala	Asn	Ile
				215					220					225
Ser	Met	Gly	Val	His	Phe	His	Lys	Val	Thr	Asn	Asn	Glu	Phe	Arg
				230					235					240
Val	Pro	Val	Leu	Leu	Thr	Ala	Gly	Gly	Leu	Ala	Pro	Asp	Asn	Leu
				245					250					255
Phe	Ala	Ile	Val	Lys	Leu	Ser	Ile	Cys	His	Phe	Gly	Leu	Glu	Phe
				260					265					270
Gly	Tyr	Arg	Val	Ser	Phe									
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<210> 45

<211> 813

<212> DNA

<213> *Ehrlichia canis*

<220>

<223> nucleic acid sequence of *E. canis* p28-9

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gttaggtctt gataagtctg agataaatac tcacagcaat ttacacgat  250
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ggatattatg ttaatgactt tagggtagaa tttgaaggtt cttatgagaa 350

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tagaaatagc ttaccatcct actgcattat ctgacgttcc tagaactact 750
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<210>      46
<211>      271
<212>      PRT
<213>      Ehrlichia canis

<220>
<223>      amino acid sequence of E. canis p28-9 protein

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<400>      46
Met Asn Tyr Lys Arg Phe Val Val Gly Val Thr Leu Ser Thr Phe
          5              10              15
Val Phe Phe Leu Ser Asp Gly Ala Phe Ser Asp Ala Asn Phe Ser
          20              25              30
Glu Gly Arg Arg Gly Leu Tyr Ile Gly Ser Gln Tyr Lys Val Gly
          35              40              45
Ile Pro Asn Phe Ser Asn Phe Ser Ala Glu Glu Thr Ile Pro Gly
          50              55              60
Ile Thr Lys Lys Ile Phe Ala Leu Gly Leu Asp Lys Ser Glu Ile
          65              70              75
Asn Thr His Ser Asn Phe Thr Arg Ser Tyr Asp Pro Thr Tyr Ala
          80              85              90
Ser Ser Phe Ala Gly Phe Ser Gly Ile Ile Gly Tyr Tyr Val Asn
          95              100             105

```

Asp	Phe	Arg	Val	Glu	Phe	Glu	Gly	Ser	Tyr	Glu	Asn	Phe	Glu	Pro
				110					115					120
Glu	Arg	Gln	Trp	Tyr	Pro	Glu	Asn	Ser	Gln	Ser	Tyr	Lys	Phe	Phe
				125					130					135
Ala	Leu	Ser	Arg	Asn	Ala	Thr	Asn	Ser	Asp	Asn	Lys	Phe	Ile	Val
				140					145					150
Leu	Glu	Asn	Asn	Gly	Val	Val	Asp	Lys	Ser	Leu	Asn	Val	Asn	Val
				155					160					165
Cys	Tyr	Asp	Ile	Ala	Ser	Gly	Ser	Ile	Pro	Leu	Ala	Pro	Tyr	Met
				170					175					180
Cys	Ala	Gly	Val	Gly	Ala	Asp	Tyr	Ile	Lys	Phe	Leu	Gly	Ile	Ser
				185					190					195
Leu	Pro	Lys	Phe	Ser	Tyr	Gln	Val	Lys	Phe	Gly	Val	Asn	Tyr	Pro
				200					205					210
Leu	Asn	Val	Asn	Thr	Met	Leu	Phe	Gly	Gly	Gly	Tyr	Tyr	His	Lys
				215					220					225
Val	Val	Gly	Asp	Arg	His	Glu	Arg	Val	Glu	Ile	Ala	Tyr	His	Pro
				230					235					240
Thr	Ala	Leu	Ser	Asp	Val	Pro	Arg	Thr	Thr	Ser	Ala	Ser	Ala	Thr
				245					250					255
Leu	Asn	Thr	Asp	Tyr	Phe	Gly	Trp	Glu	Ile	Gly	Phe	Arg	Phe	Ala
				260					265					270
Leu														
271														